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#51
12-2-01
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DEC 18 2001
TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/842,347A

DATE: 12/05/2001
TIME: 10:30:46

Input Set : N:\Crf3\RULE60\09842347A.txt
Output Set: N:\CRF3\12052001\I842347A.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: TAKAHASHI, Tohru
7 SERIZAWA, Nobufusa
8 KOISHI, Ryuta
9 KAWASHIMA, Ichiro
11 (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
12 AUTOLYZING FUSION PROTEINS
13 AND A NOVEL REDUCING POLYPEPTIDE
15 (iii) NUMBER OF SEQUENCES: 19
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.
19 (B) STREET: 767 Third Avenue-25th Floor
20 (C) CITY: New York
21 (D) STATE: New York
22 (E) COUNTRY: United States
23 (F) ZIP: 10017-2023
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.24
31 (vi) CURRENT APPLICATION DATA:
C--> 32 (A) APPLICATION NUMBER: US/09/842,347A
C--> 33 (B) FILING DATE: 25-Apr-2001
34 (C) CLASSIFICATION:
43 (vii) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: 08/500,635
38 (B) FILING DATE: 1995-07-11
40 (A) APPLICATION NUMBER: JP 6-218392
41 (B) FILING DATE: 13-SEP-1994
44 (A) APPLICATION NUMBER: JP 6-303809
45 (B) FILING DATE: 07-DEC-1994
47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Goodman, Herbert
49 (B) REGISTRATION NUMBER: 17081
50 (C) REFERENCE/DOCKET NUMBER: 950376/HG
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: (212) 319-4900
54 (B) TELEFAX: (212) 319-5101
55 (C) TELEX: 236268
58 (2) INFORMATION FOR SEQ ID NO: 1:
60 (i) SEQUENCE CHARACTERISTICS:
61 (A) LENGTH: 1320 base pairs
62 (B) TYPE: nucleic acid
63 (C) STRANDEDNESS: double
64 (D) TOPOLOGY: linear

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66      (ii) MOLECULE TYPE: cDNA to mRNA
W--> 68      (iii) HYPOTHETICAL: N
W--> 70      (iv) ANTI-SENSE: N
72      (vi) ORIGINAL SOURCE:
73          (A) ORGANISM: Clover Yellow Vein Virus
75      (ix) FEATURE:
76          (A) NAME/KEY: CDS
77          (B) LOCATION: 1..1320
78          (D) OTHER INFORMATION:
79      (ix) FEATURE:
80          (A) NAME/KEY: mat_peptide
81          (B) LOCATION: 10..1311
82          (D) OTHER INFORMATION:
86      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
88 AAG TTC CAA GGG AAA AGT AAG AGA ACA AGA CAA AAG TTG AAG TTC AGA      48
89 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
90 1      5      10      15
92 GCG GCA AGA GAC ATG AAG GAT CGT TAT GAA GTG CAT GCC GAT GAG GGG      96
93 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
94      20      25      30
96 ACT TTA GTG GAA AAT TTT GGA ACT CGT TAT TCA AAG AAA GGC AAG ACA      144
97 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
98      35      40      45
100 AAA GGT ACT GTT GTG GGT TTG GGT GCA AAA ACA AGA CGG TTC ACT AAC      192
101 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
102      50      55      60
104 ATG TAT GGT TTT GAC CCC ACG GAG TAT TCA TTT GCT AGG TAT CTT GAT      240
105 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
106 65      70      75      80
108 CCA ATC ACG GGT GCA ACA TTG GAT GAA ACC CCA ATT CAC AAT GTA AAT      288
109 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
110      85      90      95
112 TTG GTT GCT GAG CAT TTT GGC GAC ATA AGG CTT GAT ATG GTT GAC AAG      336
113 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
W--> 114      100      105      110
116 GAG TTA CTT GAC AAA CAG CAC TTA TAC CTC AAG AGA CCA ATA GAA TGT      384
117 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
W--> 118      115      120      125
120 TAC TTT GTA AAG GAT GCT GGT CAG AAG GTG ATG AGG ATT GAT CTA ACA      432
121 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
W--> 122      130      135      140
124 CCC CAC AAC CCA TTG TTG GCA AGC GAT GTT AGC ACA ACC ATA ATG GGT      480
125 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
W--> 126 145      150      155      160
128 TAT CCT GAG AGA GAA GGT GAA CTC CGT CAA ACT GGA AAG GCA AGG TTA      528
129 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
W--> 130      165      170      175
132 GTC GAC CCA TCA GAG TTG CCC GCG CGG AAT GAG GAT ATT GAT GCA GAG      576
133 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu

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W--> 134          180          185          190
      136 TTT GAG AGT CTA AAT CGC ATA AGT GGT TTG CGC GAC TAT AAT CCC ATT      624
      137 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
W--> 138          195          200          205
      140 TCA CAA AAT GTT TGC TTG CTA ACA AAT GAG TCA GAA GGC CAT AGA GAG      672
      141 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
W--> 142          210          215          220
      144 AAG ATG TTT GGA ATT GGA TAT GGT TCA GTG ATC ATT ACA AAT CAA CAT      720
      145 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
W--> 146 225          230          235          240
      148 CTG TTC AGA AGG AAT AAT GGG GAG TTA TCA ATT CAA TCC AAG CAT GGC      768
      149 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
W--> 150          245          250          255
      152 TAC TTC AGA TGC CGC AAC ACC ACA AGC TTG AAG ATG CTG CCT TTG GAG      816
      153 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
W--> 154          260          265          270
      156 GGA CAT GAC ATT TTG TTG ATT CAG TTA CCA AGG GAC TTT CCA GTG TTT      864
      157 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
W--> 158          275          280          285
      160 CCA CAA AAG ATT CGC TTT AGG GAG CCA AGA GTG GAT GAC AAA ATT GTT      912
      161 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
W--> 162          290          295          300
      164 TTG GTC AGC ACA AAT TTC CAG GAA AAG AGT TCC TCG AGC ACG GTC TCA      960
      165 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Thr Val Ser
W--> 166 305          310          315          320
      168 GAG TCC AGT AAC ATT TCA AGA GTG CAG TCA GCC AAT TTC TAC AAG CAT     1008
      169 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
W--> 170          325          330          335
      172 TGG ATC TCA ACA GTA GCA GGA CAC TGT GGA AAC CCT ATG GTT TCG ACT     1056
      173 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
W--> 174          340          345          350
      176 AAA GAT GGA TTT ATT GTA GGT ATC CAC AGT CTT GCT TCA TTG ACA GGC     1104
      177 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
W--> 178          355          360          365
      180 GAC GTT AAC ATC TTC ACA AGC TTT CCG CCG CAG TTT GAG AAC AAA TAT     1152
      181 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
W--> 182          370          375          380
      184 CTA CAG AAG CTC AGT GAA CAC ACA TGG TGT AGT GGA TGG AAA CTA AAT     1200
      185 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
W--> 186 385          390          395          400
      188 CTT GGA AAG ATT AGT TGG GGT GGA ATC AAC ATT GTG GAG GAT GCA CCT     1248
      189 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
W--> 190          405          410          415
      192 GAA GAG CCC TTT ATA ACA TCC AAG ATG GCA AGC CTT CTT AGT GAT TTG     1296
      193 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
W--> 194          420          425          430
      196 AAT TGT TCA TTC CAA GCA AGT GCG                                     1320
      197 Asn Cys Ser Phe Gln Ala Ser Ala
W--> 198          435          440

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201 (2) INFORMATION FOR SEQ ID NO: 2:

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 440 amino acids

205 (B) TYPE: amino acid

206 (D) TOPOLOGY: linear

208 (ii) MOLECULE TYPE: protein

210 (vi) ORIGINAL SOURCE:

211 (A) ORGANISM: Clover Yellow Vein Virus

213 (ix) FEATURE:

214 (A) NAME/KEY: mat_peptide

215 (B) LOCATION: 4..437

216 (D) OTHER INFORMATION:

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

221 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg
222   1           5           10           15
224 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly
225           20           25           30
227 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr
228           35           40           45
230 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn
231           50           55           60
233 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp
234   65           70           75           80
236 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn
237           85           90           95
239 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys
240           100          105          110
242 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys
243           115          120          125
245 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr
246           130          135          140
248 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly
249 145           150          155          160
251 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu
252           165          170          175
254 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu
255           180          185          190
257 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile
258           195          200          205
260 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu
261           210          215          220
263 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His
264 225           230          235          240
266 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly
267           245          250          255
269 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu
270           260          265          270
272 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe
273           275          280          285

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275 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val
276      290      295      300
278 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Thr Val Ser
279 305      310      315      320
281 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His
282      325      330      335
284 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr
285      340      345      350
287 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly
288      355      360      365
290 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr
291      370      375      380
293 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn
294 385      390      395      400
296 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro
297      405      410      415
299 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu
300      420      425      430
302 Asn Cys Ser Phe Gln Ala Ser Ala
303      435      440

```

305 (2) INFORMATION FOR SEQ ID NO: 3:

307 (i) SEQUENCE CHARACTERISTICS:

308 (A) LENGTH: 25 base pairs

309 (B) TYPE: nucleic acid

310 (C) STRANDEDNESS: single

311 (D) TOPOLOGY: linear

313 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

W--> 315 (iii) HYPOTHETICAL: N

W--> 317 (iv) ANTI-SENSE: N

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

323 GTCCATGGGG AAAAGTAAGA GAACA

325 (2) INFORMATION FOR SEQ ID NO: 4:

327 (i) SEQUENCE CHARACTERISTICS:

328 (A) LENGTH: 20 base pairs

329 (B) TYPE: nucleic acid

330 (C) STRANDEDNESS: single

331 (D) TOPOLOGY: linear

333 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

W--> 335 (iii) HYPOTHETICAL: N

W--> 337 (iv) ANTI-SENSE: N

341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

343 ACTCTGAGAC CGTGCTCGAG

345 (2) INFORMATION FOR SEQ ID NO: 5:

347 (i) SEQUENCE CHARACTERISTICS:

348 (A) LENGTH: 20 base pairs

349 (B) TYPE: nucleic acid

350 (C) STRANDEDNESS: single

351 (D) TOPOLOGY: linear

353 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

25

20

VERIFICATION SUMMARY

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TIME: 10:30:47

Input Set : N:\Crf3\RULE60\09842347A.txt

Output Set: N:\CRF3\12052001\I842347A.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:68 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1
L:70 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:315 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3
L:317 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3
L:335 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=4
L:337 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=4
L:355 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5
L:357 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5
L:375 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=6
L:377 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=6
L:395 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7
L:397 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7
L:415 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=8
L:417 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=8
L:435 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=10
L:473 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11
L:768 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13
L:770 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13
L:788 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=14
L:790 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=14
L:810 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15
L:812 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15

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L:830 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=16
L:832 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=16
L:850 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=17
L:852 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=17
L:870 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=18
L:872 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=18
L:893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19